Usually, I find it really necessary to conduct editing and proofreading for clarity first:

Original text	Edits (highlighted parts are edited)
On the other hand, medium components might also have an effect on secreted proteins, more particularly on their glycosylation, which is essential for their bioactivity and stability in vivo. The traditional strategy used for medium development, relying on the variation of one factor at a time (OFAT) while keeping the others constant, is laborious and time-consuming and does not account for synergistic interactions of components. Therefore, new technologies such, as design of experiments (DoE) and statistical analyses, which enable the testing of several components at a time and identification of their interactions, have been implemented. Several strategies for medium optimization have been described. For example, optimization can be based on spent medium analysis, on metabolite flux analyses or on metabolomics, allowing rebalance of components in subsequent experiments. On the other hand, in the high-throughput approach where statistical DoE is linked to automation and small cell culture devices enable testing of several hundreds of media formulations, tests are usually performed by monitoring critical process outputs, e.g., cell growth, protein titers. When working with complex biological systems such as recombinant mammalian cell cultures, mixture designs to evaluate combinations of different defined formulations can be an important tool for media optimization. This approach is particularly interesting when testing numerous components because it avoids component solubility issues that might occur using factorial designs. Through evaluation of the performance of the various new mixtures obtained by media blending, optimal concentration ranges of the various medium components can be identified. Jordan et al. recently described a novel high throughput methodology based on an extended media blending strategy that was used to reshuffle 20 amino acids in one round of experiments. Several significantly improved viable cell densities and titers of a Chinese hamster ovary (CHO) cell batch culture producing a monoclonal antibody (mAb)	On the one hand, medium components might also have an effect on secreted proteins, more particularly on their glycosylation. Such glycosylation is essential for their bioactivity and stability in vivo. The traditional strategy used for medium development relies on the variation of one factor at a time (OFAT) while keeping the others constant. The traditional strategy is laborious and time-consuming and does not account for synergistic interactions of components. Therefore, new technologies, such as design of experiments (DoE) and statistical analyses have been implemented. These technologies enable the testing of several components at a time and identification of their interactions. Several strategies for medium optimization have been described. For example, optimization can be based on spent medium analysis, on metabolite flux analyses or on metabolomics, allowing rebalance of components in subsequent experiments. On the other hand, the high-throughput approach, where statistical DoE is linked to automation and small cell culture devices, enable testing of several hundreds of media formulations. The tests are usually performed by monitoring critical process outputs, e.g., cell growth, protein titers. When working with complex biological systems, such as recombinant mammalian cell cultures, mixture designs to evaluate combinations of differently defined formulations can be an important tool for media optimization. This approach is particularly interesting when testing numerous components because it avoids component solubility issues that might occur using factorial designs. Through evaluation of the performance of the various new mixtures obtained by media blending, optimal concentration ranges of the various medium components can be identified. Jordan et al. recently described a novel high throughput methodology based on an extended media blending strategy that was used to reshuffle 20 amino acids in one round of experiments. They prepared 192 mixtures by blending media from 10 formulations and

resulted from 192 mixtures prepared by media blending from 10 formulations.	resulted in several significantly improved viable cell densities and titers of a Chinese hamster ovary (CHO) cell batch culture, producing a monoclonal antibody (mAb).

After the editing, the translation can be conducted easily:

Edits (highlighted parts are edited)	Translation
On the one hand, medium components might also have an effect on secreted proteins, more particularly on their glycosylation. Such glycosylation is essential for their bioactivity and stability in vivo. The traditional strategy used for medium development relies on the variation of one factor at a time (OFAT) while keeping the others constant. The traditional strategy is laborious and time-consuming and does not account for synergistic interactions of components. Therefore, new technologies, such as design of experiments (DoE) and statistical analyses have been implemented. These technologies enable the testing of several components at a time and identification of their interactions. Several strategies for medium optimization have been described. For example, optimization can be based on spent medium analysis, on metabolite flux analyses or on metabolomics, allowing rebalance of components in subsequent experiments. On the other hand, the high-throughput approach, where statistical DoE is linked to automation and small cell culture devices, enable testing of several hundreds of media formulations. The tests are usually performed by monitoring critical process outputs, e.g., cell growth, protein titers. When working with complex biological systems, such as recombinant mammalian cell cultures, mixture designs to evaluate combinations of differently defined formulations can be an important tool for media optimization. This approach is particularly interesting when testing numerous components because it avoids component solubility issues that might occur using factorial designs. Through evaluation of the performance of the various new mixtures obtained by media blending, optimal concentration ranges of the various medium components can be identified. Jordan et al. recently described a novel high throughput methodology based on an extended media blending strategy that was used to reshuffle 20 amino acids in one round of experiments. They prepared 192 mixtures by blending media from 10 formulations	一方面，培养基成分也可能对分泌的蛋白质，特别是对其糖基化有影响。此类糖基化对其生物活性和体内稳定性至关重要。用于培养基开发的传统策略依赖于一次改变一个因素（OFAT）、同时保持其他因素不变的方案。传统的策略既费力又费时，并且不考虑组件之间的协同相互作用。因此，科研人员已经实施了新技术，例如实验设计（DoE）和统计分析。这些技术可以一次测试多个组件并确定它们之间的相互作用。已经描述了几种用于培养基优化的策略。例如，可以基于用过的培养基分析、代谢物通量分析或代谢组学进行优化，从而可以在后续实验中重新平衡组分。另一方面，通过统计 DoE 与自动化和小型细胞培养设备相关联的高通量方法，可以测试数百种培养基配方。这些测试通常通过监测关键的过程输出来进行测试，例如细胞生长，蛋白质滴度。与复杂的生物系统（例如重组哺乳动物细胞培养物）一起使用时，用于评估不同定义制剂组合的混合物设计可能是培养基优化的重要工具。当测试大量组件时，此方法特别有趣，因为它避免了使用析因设计时可能发生的组件溶解性问题。通过评估通过介质混合获得的各种新混合物的性能，可以确定各种介质组分的最佳浓度范围。最近，Jordan 等人描述了一种全新的、基于扩展媒体混合策略的高通量方法，该方法能够在在一轮实验中对 20 个氨基酸进行改组。他们通过混合 10 种配方的培养基制备了 192 种混合物，并显着提高了中国仓鼠卵巢

and resulted in several significantly improved viable cell densities and titers of a Chinese hamster ovary (CHO) cell batch culture, producing a monoclonal antibody (mAb).	（CHO）细胞分批培养的活细胞密度和滴度，产生了单克隆抗体（mAb）。